

Supplementary Table S15. Methylation change by polycomb status in MDS models and human MDS patients.

Mouse MDS models			All genes		PHC1		RNF2		SUZ12		EED		H3K27me3		SUZ12/EED	
			targets	non-targets	targets	non-targets	targets	non-targets	targets	non-targets	targets	non-targets	targets	non-targets		
RUNX1	Hypermethylated genes	log2>1	Genes	3302	359	2943	437	2865	468	2834	321	2981	842	2460	303	2999
			Genes	428	145	283	155	273	186	242	139	289	255	173	135	293
			%	13.0%	40.4%	9.6%	35.5%	9.5%	39.7%	8.5%	43.3%	9.7%	30.3%	7.0%	44.6%	9.8%
	Fold change		4.2		3.7		4.7		4.5		4.3		4.6			
	Hypomethylated genes	log2<-1	Genes	84	1	83	7	77	3	81	1	83	11	73	0	84
			%	2.5%	0.3%	2.8%	1.6%	2.7%	0.6%	2.9%	0.3%	2.8%	1.3%	3.0%	0.0%	2.8%
Fold change			0.1		0.6		0.2		0.1		0.4		0.0			
NHD13	Hypermethylated genes	log2>1	Genes	484	80	404	88	396	97	387	67	417	152	332	65	419
			%	14.7%	22.3%	13.7%	20.1%	13.8%	20.7%	13.7%	20.9%	14.0%	18.1%	13.5%	21.5%	14.0%
			Fold change		1.6		1.5		1.5		1.5		1.3		1.5	
	Hypomethylated genes	log2<-1	Genes	186	13	173	17	169	13	173	9	177	38	148	6	180
			%	5.6%	3.6%	5.9%	3.9%	5.9%	2.8%	6.1%	2.8%	5.9%	4.5%	6.0%	2.0%	6.0%
			Fold change		0.6		0.7		0.5		0.5		0.8		0.3	

Human MDS patients			All genes	SUZ12		EED		H3K27me3		SUZ12/EED		
				targets	non-targets	targets	non-targets	targets	non-targets	targets	non-targets	
MDS (7/19)	Hypermethylated genes	log2>1	Genes	8478	681	7797	682	7796	750	7728	507	7971
			Genes	615	165	450	169	446	171	444	136	479
			%	7.3%	24.2%	5.8%	24.8%	5.7%	22.8%	5.7%	26.8%	6.0%
	Hypomethylated genes	log2<-1	Fold change	4.2		4.3		4.0		4.5		
			Genes	92	3	89	6	86	6	86	3	89
			%	1.1%	0.4%	1.1%	0.9%	1.1%	0.8%	1.1%	0.6%	1.1%
			Fold change	0.4		0.8		0.7		0.5		